



FIGURE 1A

Amino acid sequence for full-length human wild type AKT3 [SEQ. ID No. 1]

(Residues 136-461 are underlined)

MSDVTIVKEG	WVQKRGEYIK	NWRPRYFLK	TDGSFIGYKE	KPQDVDLPYP	LNNFSVAKCQ	60
LMKTERPKPN	TFIIRCLQWT	TVIERTFHVD	TPEEREWTE	AIQAVADRLQ	RQEEERMNCS	120
PTSQIDNIGE	EEMDASTTHH	KRKTMNDFDY	LKLLGKGTFG	KVILVREKAS	GKYYAMKILK	180
KEVIIAKDEV	AHTLTESRVL	KNTRHPFLTS	LKYSFQTKDR	LCFVMEYVNG	GELFFHLSRE	240
RVFSEDRTRF	YGAEIVSALD	YLHSGKIVYR	DLKLENLMLD	KDGHIKITDF	GLCKEGITDA	300
ATMKTFCGTP	EYLAPEVLED	NDYGRAVDWW	GLGVVMYEMM	CGRLPFYNQD	HEKLFELILM	360
EDIKFPRTL	SDAKSLLSGL	LIKDPNKRLG	GGPDDAKEIM	RHSFFSGVNW	QDVYDKKLVP	420
FPKPQVTSET	DTRYFDEEFT	AQTITITPPE	KYDEDEGMDCM	DNERRPHFPQ	FSYSASGRE	479

Human cDNA sequence encoding residues 136-461 of AKT3 [SEQ. ID No. 2]

TCTACAACCC	ATCATAAAAG	AAAGACAATG	AATGATTTTG	ACTATTTGAA	ACTACTAGGT	60
AAAGGCACCT	TTGGGAAAAGT	TATTTTGGTT	CGAGAGAAGG	CAAGTGGAAA	ATACTATGCT	120
ATGAAGATTC	TGAAGAAAGA	AGTCATTATT	GCAAAGGATG	AAGTGGCACA	CACCTCTAAT	180
GAAAGCAGAG	TATTAAAGAA	CACTAGACAT	CCCTTTTAA	CATCCTTGAA	ATATTCCTTC	240
CAGACAAAAG	ACCGTTTGTG	TTTTGTGATG	GAATATGTTA	ATGGGGGCGA	GCTGTTTTTC	300
CATTTGTCTGA	GAGAGCGGGT	GTTCTCTGAG	GACCGCACAC	GTTTCTATGG	TGCAGAAATT	360
GTCTCTGCCCT	TGGACTATCT	ACATTCGGGA	AAGATTGTGT	ACCGTGATCT	CAAGTTGGAG	420
AATCTAATGC	TGGACAAAGA	TGGCCACATA	AAAATTACAG	ATTTTGGACT	TTGCAAAGAA	480
GGGATCACAG	ATGCAGCCAC	CATGAAGACA	TTCTGTGGCA	CTCCAGAATA	TCTGGCACCA	540
GAGGTGTTAG	AAGATAATGA	CTATGGCCGA	GCAGTAGACT	GGTGGGGCCT	AGGGGTTGTC	600
ATGTATGAAA	TGATGTGTGG	GAGGTTACCT	TTCTACAACC	AGGACCATGA	GAAACTTTTT	660
GAATTAATAT	TAATGGAAGA	CATTAAATTT	CCTCGAACAC	TCTCTTCAGA	TGCAAAATCA	720
TTGCTTTTCAG	GGCTCTTGAT	AAAGGATCCA	AATAAACGCC	TTGGTGGAGG	ACCAGATGAT	780
GCAAAAGAAA	TTATGAGACA	CAGTTTCTTC	TCTGGAGTAA	ACTGGCAAGA	TGTATATGAT	840
AAAAAGCTTG	TACCTCCTTT	TAAACCTCAA	GTAACATCTG	AGACAGATAC	TAGATATTTT	900
GATGAAGAAT	TTACAGCTCA	GACTATTACA	ATAACACCAC	CTGAAAAATA	TGATGAGGAT	960
GGTATGGACT	GCATGGAC					978

FIGURE 1B

Amino acid sequence for residues 136-461 of AKT3 with a cleavable

N-terminal intein tag [SEQ. ID No. 3]

(N-terminal intein tag and cleavage site are underlined. The intein tag was subsequently cleaved resulting in CRSL (residues 227-230 of SEQ. ID No. 3) fused to the N-terminal of amino acids 136-461 of SEQ. ID No. 1)

<u>MKIEEGKLTN</u>	<u>PGVSAWQVNT</u>	<u>AYTAGQLVTY</u>	<u>NGKTYKCLQP</u>	<u>HTSLAGWEPS</u>	<u>NVPALWQLQN</u>	60
<u>NGNNGLELRE</u>	<u>SGAISGDSLI</u>	<u>SLASTGKRVS</u>	<u>IKDLLDEKDF</u>	<u>EIWAINQTM</u>	<u>KLES AKVSRV</u>	120
<u>FCTGKKLVYI</u>	<u>LKTRLGRTIK</u>	<u>ATANHRFLT</u>	<u>DGWKRLDELS</u>	<u>LKEHIALPRK</u>	<u>LESSSLQLSP</u>	180
<u>EIEKLSQSDI</u>	<u>YWDSIVSITE</u>	<u>TGVEEVFDLT</u>	<u>VPGPHNFVAN</u>	<u>DIIVHNCRL</u>	<u>STTHHKRKT</u>	240
<u>NDFDYLKLLG</u>	<u>KGTFGKVILV</u>	<u>REKASGKYA</u>	<u>MKILKKEVII</u>	<u>AKDEVAHTLT</u>	<u>ESRVLKNTRH</u>	300
<u>PFLTSLKYSF</u>	<u>QTKDRLCFVM</u>	<u>EYVNGGELFF</u>	<u>HLSRERVFSE</u>	<u>DRTRFYGAEI</u>	<u>VSALDYLHSG</u>	360
<u>KIVYRDLKLE</u>	<u>NLMLDKDGH</u>	<u>KITDFGLCKE</u>	<u>GITDAATMKT</u>	<u>FCGTPEYLAP</u>	<u>EVLEDNDYGR</u>	420
<u>AVDWWGLGVV</u>	<u>MYEMMCGRLP</u>	<u>FYNQDHEKLF</u>	<u>ELILMEDIKF</u>	<u>PRTLSSDAKS</u>	<u>LLSGLLIKDP</u>	480
<u>NKRLGGGPDD</u>	<u>AKEIMRHSFF</u>	<u>SGVNWQDVYD</u>	<u>KKLVPPFKPQ</u>	<u>VTSETDTRYF</u>	<u>DEEFTAQTIT</u>	540
<u>ITPPEKYDED</u>	<u>GMDCMD</u>					556

Amino acid sequence for residues 227-556 of SEQ. ID No. 3

[SEQ. ID No. 4]

<u>CRSLSTTHHK</u>	<u>RKTMNDFDYL</u>	<u>KLLGKGTFGK</u>	<u>VILVREKASG</u>	<u>KYYAMKILKK</u>	<u>EVIIAKDEVA</u>	60
<u>HTLTESRVLK</u>	<u>NTRHPFLTSL</u>	<u>KYSFQTKDRL</u>	<u>CFVMEYVNGG</u>	<u>ELFFHLSRER</u>	<u>VFSEDRTRFY</u>	120
<u>GAEIVSALDY</u>	<u>LHSGKIVYRD</u>	<u>LKLENLMLDK</u>	<u>DGHIKITDFG</u>	<u>LCKEGITDAA</u>	<u>TMKTFCGTPE</u>	180
<u>YLAPEVLEDN</u>	<u>DYGRAVDWWG</u>	<u>LGVMYEMMC</u>	<u>GRLPFYNQDH</u>	<u>EKLFEILIME</u>	<u>DIKFPRTLSS</u>	240
<u>DAKSLLSGLL</u>	<u>IKDPNKRLGG</u>	<u>GPDDAKEIMR</u>	<u>HSFFSGVNWQ</u>	<u>DVYDKKLVPP</u>	<u>FKPQVTSETD</u>	300
<u>TRYFDEEFTA</u>	<u>QTITITPPEK</u>	<u>YDEDGMDCMD</u>				360

FIGURE 5

